

09/622439

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1/24

SEQUENCE LIST

<110> Yamanouchi Pharmaceutical Co., Ltd.

<120> A novel G protein coupled receptor protein

<130> Y9905-PCT

<150> JP P1998-060245

<151> 1998-03-12

<150> JP P1999-026774

<151> 1999-02-03

<160> 26

<170> PatentIn Ver. 2.0

<210> 1

<211> 1128

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (1125)

<223> SREB1

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 1 5 10 15

gcc ctg ggc ctc aag ctg gcc acg ctc agc ctg ctg ctg tgc gtg agc 96
 Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser
 20 25 30

cta gcg ggc aac gtg ctg ttc gcg ctg ctg atc gtg cgc gag cgc agc 144
 Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser
 35 40 45

ctg cac cgc gcc ccg tac tac ctg ctg ctc gac ctg tgc ctg gcc gac 192
 Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp
 50 55 60

ggg ctg cgc gcg ctc gcc tgc ctc ccg gcc gtc atg ctg gcg gcg cgc 240
 Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg
 65 70 75 80

cgt gcg gcg gcc gcg gcg ggg gcg ccg ccg ggc gcg ctg ggc tgc aag 288
 Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys
 85 90 95

ctg ctc gcc ttc ctg gcc gcg ctc ttc tgc ttc cac gcc gcc ttc ctg 336
 Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu
 100 105 110

2/24

00662430-081700

ctg ctg ggc gtg ggc gtc Leu Leu Gly Val Gly Val 115	acc cgc tac ctg gcc atc gcg cac cac cgc Thr Arg Tyr Leu Ala Ile Ala His His Arg 120	384
ttc tat gca gag cgc ctg Phe Tyr Ala Glu Arg Leu 130	gcc ggc tgg ccg tgc gcc gcc atg ctg gtg Ala Gly Trp Pro Cys Ala Ala Met Leu Val 135	432
tgc gcc gcc tgg gcg ctg Cys Ala Ala Trp Ala Leu 145	gcg ctg gcc gcg gcc ttc ccg cca gtg ctg Ala Leu Ala Ala Ala Phe Pro Pro Val Leu 150	480
gac ggc ggt ggc gac gac Asp Gly Gly Gly Asp 165	gag gac gcg ccg tgc gcc ctg gag cag cgg Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg 170	528
ccc gac ggc gcc ccc ggc Pro Asp Gly Ala Pro Gly 180	gcg ctg ggc ttc ctg ctg ctg ctg gcc gtg Ala Leu Gly Phe Leu Leu Leu Leu Ala Val 185	576
gtg gtg ggc gcc acg cac Val Val Gly Ala Thr His 195	ctc gtc tac ctc cgc ctg ctc ttc ttc atc Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile 200	624
cac gac cgc cgc aag atg His Asp Arg Arg Lys Met 210	cgg ccc gcg cgc ctg gtg ccc gcc gtc agc Arg Pro Ala Arg Leu Val Pro Ala Val Ser 215	672
cac gac tgg acc ttc cac His Asp Trp Thr Phe His 225	ggc ccg ggc gcc acc ggc cag gcg gcc gcc Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala 230	720
aac tgg acg gcg ggc ttc Asn Trp Thr Ala Gly Phe 245	ggc cgc ggc ccc acg ccg ccc gcg ctt gtg Gly Arg Gly Pro Thr Pro Pro Ala Leu Val 250	768
ggc atc cgg ccc gca ggc Gly Ile Arg Pro Ala Gly 260	ccg ggc cgc ggc gcg cgc cgc ctc ctc gtg Pro Gly Arg Gly Ala Arg Arg Leu Leu Val 265	816
ctg gaa gaa ttc aag acg Leu Glu Glu Phe Lys Thr 275	gag aag agg ctg tgc aag atg ttc tac gcc Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala 280	864
gtc acg ctg ctc ttc ctg Val Thr Leu Leu Phe Leu 290	ctc ctc tgg ggc ccc tac gtc gtg gcc agc Leu Leu Trp Gly Pro Tyr Val Val Ala Ser 295	912
tac ctg cgg gtc ctg gtg Tyr Leu Arg Val Leu Val 305	cgg ccc ggc gcc gtc ccc cag gcc tac ctg Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu 310	960
acg gcc tcc gtg tgg ctg Thr Ala Ser Val Trp Leu 325	acc ttc gcg cag gcc ggc atc aac ccc gtc Thr Phe Ala Gln Ala Gly Ile Asn Pro Val 330	1008

3/24

gtg tgc ttc ctc ttc aac agg gag ctg agg gac tgc ttc agg gcc cag 1056
 Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln
 340 345 350

ttc ccc tgc tgc cag agc ccc cgg acc acc cag gcg acc cat ccc tgc 1104
 Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys
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gac ctg aaa ggc att ggt tta tga 1128
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 370 375

<210> 2
 <211> 375
 <212> PRT
 <213> Homo sapiens

<400> 2
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 20 25 30

Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser
 35 40 45

Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp
 50 55 60

Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg
 65 70 75 80

Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys
 85 90 95

Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu
 100 105 110

Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg
 115 120 125

Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val
 130 135 140

Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu
 145 150 155 160

Asp Gly Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg
 165 170 175

Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu Ala Val
 180 185 190

004130-02122900

4/24

Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile
195 200 205

His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser
210 215 220

His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala
225 230 235 240

Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val
245 250 255

Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val
260 265 270

Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala
275 280 285

Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser
290 295 300

Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu
305 310 315 320

Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val
325 330 335

Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln
340 345 350

Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys
355 360 365

Asp Leu Lys Gly Ile Gly Leu
370 375

<210> 3
<211> 1113
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1).. (1110)
<223> SREB2

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1 5 10 15

cct cta aca gcc ttt ctg aaa ctg act tcc ttg ggt ttc ata ata gga 96
Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
20 25 30

5/24

gtc agc gtg gtg ggc aac ctc ctg atc tcc att ttg cta gtg aaa gat 144
 Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35 40 45

aag acc ttg cat aga gca cct tac tac ttc ctg ttg gat ctt tgc tgt 192
 Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50 55 60

tca gat atc ctc aga tct gca att tgt ttc cca ttt gtg ttc aac tct 240
 Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65 70 75 80

gtc aaa aat ggc tct acc tgg act tat ggg act ctg act tgc aaa gtg 288
 Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85 90 95

att gcc ttt ctg ggg gtt ttg tcc tgt ttc cac act gct ttc atg ctc 336
 Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
 100 105 110

ttc tgc atc agt gtc acc aga tac tta gct atc gcc cat cac cgc ttc 384
 Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
 115 120 125

tat aca aag agg ctg acc ttt tgg acg tgt ctg gct gtg atc tgt atg 432
 Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
 130 135 140

gtg tgg act ctg tct gtc gcc atg gca ttt ccc ccg gtt tta gac gtg 480
 Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
 145 150 155 160

ggc act tac tca ttc att agg gag gaa gat caa tgc acc ttc caa cac 528
 Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His
 165 170 175

cgc tcc ttc agg gct aat gat tcc tta gga ttt atg ctg ctt ctt gct 576
 Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala
 180 185 190

ctc atc ctc cta gcc aca cag ctt gtc tac ctc aag ctg ata ttt ttc 624
 Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe
 195 200 205

gtc cac gat cga aga aaa atg aag cca gtc cag ttt gta gca gca gtc 672
 Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
 210 215 220

agc cag aac tgg act ttt cat ggt cct gga gcc agt ggc cag gca gct 720
 Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
 225 230 235 240

gcc aat tgg cta gca gga ttt gga agg ggt ccc aca cca ccc acc ttg 768
 Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu
 245 250 255

004730-081700

6/24

ctg ggc atc agg caa aat gca aac acc aca ggc aga aga agg cta ttg 816
 Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
 260 265 270

gtc tta gac gag ttc aaa atg gag aaa aga atc agc aga atg ttc tat 864
 Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
 275 280 285

ata atg act ttt ctg ttt cta acc ttg tgg ggc ccc tac ctg gtg gcc 912
 Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
 290 295 300

tgt tat tgg aga gtt ttt gca aga ggg cct gta gta cca ggg gga ttt 960
 Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
 305 310 315 320

cta aca gct gct gtc tgg atg agt ttt gcc caa gca gga atc aat cct 1008
 Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
 325 330 335

ttt gtc tgc att ttc tca aac agg gag ctg agg cgc tgt ttc agc aca 1056
 Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr
 340 345 350

acc ctt ctt tac tgc aga aaa tcc agg tta cca agg gaa cct tac tgt 1104
 Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys
 355 360 365

gtt ata tga 1113
 Val Ile
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<210> 4
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 4
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 1 5 10 15

Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
 20 25 30

Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35 40 45

Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50 55 60

Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65 70 75 80

Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85 90 95

7/24

Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
100 105 110

Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
115 120 125

Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
130 135 140

Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
145 150 155 160

Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His
165 170 175

Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala
180 185 190

Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe
195 200 205

Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
210 215 220

Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
225 230 235 240

Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu
245 250 255

Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
260 265 270

Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
275 280 285

Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
290 295 300

Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
305 310 315 320

Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
325 330 335

Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr
340 345 350

Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys
355 360 365

Val Ile
370

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8/24

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 <212> DNA
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 <222> (1).. (1119)
 <223> SREB3

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 Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
 20 25 30

atg tgc gtg agc ctg gcg ggt aac gcc atc ttg tcc ctg ctg gtg ctc 144
 Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
 35 40 45

aag gag cgt gcc ctg cac aag gct cct tac tac ttc ctg ctg gac ctg 192
 Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
 50 55 60

tgc ctg gcc gat ggc ata cgc tct gcc gtc tgc ttc ccc ttt gtg ctg 240
 Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
 65 70 75 80

gct tct gtg cgc cac ggc tct tca tgg acc ttc agt gca ctc agc tgc 288
 Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
 85 90 95

aag att gtg gcc ttt atg gcc gtg ctc ttt tgc ttc cat gcg gcc ttc 336
 Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
 100 105 110

atg ctg ttc tgc atc agc gtc acc cgc tac atg gcc atc gcc cac cac 384
 Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
 115 120 125

cgc ttc tac gcc aag cgc atg aca ctc tgg aca tgc gcg gct gtc atc 432
 Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
 130 135 140

tgc atg gcc tgg acc ctg tct gtg gcc atg gcc ttc cca cct gtc ttt 480
 Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
 145 150 155 160

gac gtg ggc acc tac aag ttt att cgg gag gag gac cag tgc atc ttt 528
 Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
 165 170 175

gag cat cgc tac ttc aag gcc aat gac acg ctg ggc ttc atg ctt atg 576

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9/24

Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
 180 185 190
 ttg gct gtg ctc atg gca gct acc cat gct gtc tac ggc aag ctg ctc 624
 Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu
 195 200 205
 ctc ttc gag tat cgt cac cgc aag atg aag cca gtg cag atg gtg cca 672
 Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro
 210 215 220
 gcc atc agc cag aac tgg aca ttc cat ggt ccc ggg gcc acc ggc cag 720
 Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln
 225 230 235 240
 gct gct gcc aac tgg atc gcc ggc ttt ggc cgt ggg ccc atg cca cca 768
 Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro
 245 250 255
 acc ctg ctg ggt atc cgg cag aat ggg cat gca gcc agc cgg cgg cta 816
 Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu
 260 265 270
 ctg ggc atg gac gag gtc aag ggt gaa aag cag ctg ggc cgc atg ttc 864
 Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe
 275 280 285
 tac gcg atc aca ctg ctc ttt ctg ctc ctc tgg tca ccc tac atc gtg 912
 Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val
 290 295 300
 gcc tgc tac tgg cga gtg ttt gtg aaa gcc tgt gct gtg ccc cac cgc 960
 Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg
 305 310 315 320
 tac ctg gcc act gct gtt tgg atg agc ttc gcc cag gct gcc gtc aac 1008
 Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn
 325 330 335
 cca att gtc tgc ttc ctg ctc aac aag gac ctc aag aag tgc ctg agg 1056
 Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Arg
 340 345 350
 act cac gcc ccc tgc tgg ggc aca gga ggt gcc ccg gct ccc aga gaa 1104
 Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu
 355 360 365
 ccc tac tgt gtc atg tga 1122
 Pro Tyr Cys Val Met
 370

<210> 6
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 <212> PRT
 <213> Homo sapiens

10/24

<400> 6

Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
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 Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
 20 25 30
 Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
 35 40 45
 Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
 50 55 60
 Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
 65 70 75 80
 Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
 85 90 95
 Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
 100 105 110
 Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
 115 120 125
 Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
 130 135 140
 Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
 145 150 155 160
 Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
 165 170 175
 Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
 180 185 190
 Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu
 195 200 205
 Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro
 210 215 220
 Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln
 225 230 235 240
 Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro
 245 250 255
 Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu
 260 265 270
 Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe
 275 280 285

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11/24

Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val
 290 295 300

Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg
 305 310 315 320

Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn
 325 330 335

Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Arg
 340 345 350

Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu
 355 360 365

Pro Tyr Cys Val Met
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<210> 7

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Forward primer

<400> 7

aaaatctaga cgcatggcg aacgcgagcg a

31

<210> 8

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:reverse primer

<400> 8

aaaatctaga gtctatgtgg cgggcctcc c

31

<210> 9

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Forward primer

<400> 9

aaaatctaga tctatggcga actatagcca tgca

34

<210> 10

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12/24

<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:reverse primer

<400> 10
aaaatctaga aaggctaaag atttacagat gctcc 35

<210> 11
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Forward primer

<400> 11
aaaatctaga gtagggcaa cactaccgga gag 33

<210> 12
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:reverse primer

<400> 12
aaaatctaga cctgtctgcc taccagcctg c 31

<210> 13
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:FLAG epitope

<400> 13
atggactaca aggacgacga tgacaagggg atcctg 36

<210> 14
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:FLAG epitope

<400> 14

002430-0242560

13/24

Met Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ile Leu
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<210> 15
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Forward primer

<400> 15
 aaaatctaga cggcgatggc gaacgctagt ga 32

<210> 16
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:reverse primer

<400> 16
 aaaatctaga cactttgaga gtcttgtaa ggc 33

<210> 17
 <211> 33
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:Forward primer

<400> 17
 aaaatctaga tctatggcga actatagcca tgc 33

<210> 18
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Forward primer

<400> 18
 aaaatctaga aaggctaaag atttacagat gctcc 35

<210> 19
 <211> 34
 <212> DNA
 <213> Artificial Sequence

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14/24

<220>

<223> Description of Artificial Sequence:reverse primer

<400> 19

aaaatctaga caaatactga actggccgat cccc

34

<210> 20

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:reverse primer

<400> 20

aaaatctaga tgttggcccc agtatggtga tcat

34

<210> 21

<211> 1134

<212> DNA

<213> Rattus sp.

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<221> CDS

<222> (1)..(1131)

<223> Rat SREB1

<400> 21

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Met	Ala	Asn	Ala	Ser	Glu	Pro	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Glu	Ala	
1				5					10					15		

gcc	gcg	ctg	ggc	ctc	agg	ctg	gcc	aca	ctc	agc	ctg	ctg	ctg	tgc	gtg	96
Ala	Ala	Leu	Gly	Leu	Arg	Leu	Ala	Thr	Leu	Ser	Leu	Leu	Leu	Cys	Val	
		20						25						30		

agc	ctg	gcg	ggc	aac	gtg	ctg	ttc	gct	ctg	ctc	atc	gtg	agg	gag	cgc	144
Ser	Leu	Ala	Gly	Asn	Val	Leu	Phe	Ala	Leu	Leu	Ile	Val	Arg	Glu	Arg	
		35						40						45		

agc	ctg	cac	cgc	gcg	cct	tac	tac	ctg	ctg	ctc	gac	ctg	tgc	ctg	gcc	192
Ser	Leu	His	Arg	Ala	Pro	Tyr	Tyr	Leu	Leu	Leu	Asp	Leu	Cys	Leu	Ala	
		50						55						60		

gac	ggg	ctg	cgc	gcg	ctc	gcc	tgt	ctc	ccg	gcc	gtc	atg	ctg	gct	gcg	240
Asp	Gly	Leu	Arg	Ala	Leu	Ala	Cys	Leu	Pro	Ala	Val	Met	Leu	Ala	Ala	
		65						70				75			80	

cgg	cgc	gcg	gca	gcc	gcg	ggc	ggg	acg	cct	ccg	ggg	gcg	ctg	ggc	tgc	288
Arg	Arg	Ala	Ala	Ala	Ala	Ala	Gly	Thr	Pro	Pro	Gly	Ala	Leu	Gly	Cys	
				85					90					95		

aag	ctg	ctg	gcc	ttc	ctg	gcc	gcg	ctc	ttc	tgc	ttc	cac	gcg	gcc	ttc	336
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

004430-084700

15/24

Lys Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe
 100 105 110

ctg ctg ctg ggc gtg ggc gtc acc cgc tac ctg gcc atc gct cac cac 384
 Leu Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His
 115 120 125

cgc ttc tat gcc gag cgc ctg gcc ggc tgg ccg tgc gcc gcg atg ctg 432
 Arg Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu
 130 135 140

gtg tgc gcc gcc tgg ggc ctg gct ttg gcc gcg gcc ttc ccg ccg gtg 480
 Val Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Phe Pro Pro Val
 145 150 155 160

ctg gac ggc ggt ggc ggc gac gac gag gat gcg ccg tgc gcc ctg gag 528
 Leu Asp Gly Gly Gly Ala Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu
 165 170 175

cag cgg ccc gac ggc gcc ccg ggt gcg cta ggc ttc ctg ctg ctc ctg 576
 Gln Arg Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu
 180 185 190

gcc gcg gtg gtg ggc gcc acg cac ctc gtc tac ctt cgc ctg ctc ttc 624
 Ala Ala Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe
 195 200 205

ttc atc cac gac cgc cgc aag atg cgg ccc gca cgc ctg gtg ccc gcc 672
 Phe Ile His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala
 210 215 220

gtc agc cac gac tgg acc ttc cac ggc ccg ggc gcc acc ggt caa gcg 720
 Val Ser His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala
 225 230 235 240

gcc gcc aac tgg acg gcg ggc ttc ggc cgc ggc ccc acg cca cct gcg 768
 Ala Ala Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala
 245 250 255

ctc gtg ggc atc agg cct gca ggc ccg ggc cgc gga gcc ccg cgc ctc 816
 Leu Val Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu
 260 265 270

ctg gtg ctg gag gaa ttc aag acg gag aag agg ctg tgc aag atg ttc 864
 Leu Val Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe
 275 280 285

tac gcc atc acg ctg ctc ttc ctg ctc ctc tgg ggc ccc tat gtg gtt 912
 Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val
 290 295 300

gcc agt tac ctg cgc gtc ctg gtg ccg ccc gga gct gtc ccg cag gcc 960
 Ala Ser Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala
 305 310 315 320

tac ctg aca gcc tgc gtg tgg ctg aca ttc gca cag gcc ggc atc aac 1008

004180-02422960

16/24

Tyr Leu Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn
 325 330 335

ccc gtg gtg tgt ttc ctc ttc aac cgg gag ctg agg gac tgt ttc aga 1056
 Pro Val Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg
 340 345 350

gcc cag ttc ccc tgt tgc cag agc ccc cag gcc acg cag gcc acc ctc 1104
 Ala Gln Phe Pro Cys Cys Gln Ser Pro Gln Ala Thr Gln Ala Thr Leu
 355 360 365

ccc tgc gac ctg aaa gcc att ggt ttg tga 1134
 Pro Cys Asp Leu Lys Gly Ile Gly Leu
 370 375

<210> 22
 <211> 377
 <212> PRT
 <213> Rattus sp.

<400> 22
 Met Ala Asn Ala Ser Glu Pro Gly Gly Gly Gly Gly Gly Ala Glu Ala
 1 5 10 15

Ala Ala Leu Gly Leu Arg Leu Ala Thr Leu Ser Leu Leu Leu Cys Val
 20 25 30

Ser Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg
 35 40 45

Ser Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala
 50 55 60

Asp Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala
 65 70 75 80

Arg Arg Ala Ala Ala Ala Ala Gly Thr Pro Pro Gly Ala Leu Gly Cys
 85 90 95

Lys Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe
 100 105 110

Leu Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His
 115 120 125

Arg Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu
 130 135 140

Val Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val
 145 150 155 160

Leu Asp Gly Gly Gly Ala Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu
 165 170 175

Gln Arg Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu

0062430-001700

17/24

180

185

190

Ala Ala Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe
195 200 205

Phe Ile His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala
210 215 220

Val Ser His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala
225 230 235 240

Ala Ala Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala
245 250 255

Leu Val Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu
260 265 270

Leu Val Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe
275 280 285

Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val
290 295 300

Ala Ser Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala
305 310 315 320

Tyr Leu Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn
325 330 335

Pro Val Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg
340 345 350

Ala Gln Phe Pro Cys Cys Gln Ser Pro Gln Ala Thr Gln Ala Thr Leu
355 360 365

Pro Cys Asp Leu Lys Gly Ile Gly Leu
370 375

<210> 23

<211> 1113

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (1)..(1110)

<223> Rat SREB2

<400> 23

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Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
1 5 10 15

cct cta aca gcc ttt ctg aaa ctg act tcc ttg ggt ttc ata ata gga 96
Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly

0062430 004700

18/24

20

25

30

gtc agt gtg gtg ggc aac ctt ctg atc tcc att ttg cta gtg aaa gat 144
 Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35 40 45

aag acc ttg cat aga gct cct tac tac ttc ctg ctg gat ctg tgc tgc 192
 Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50 55 60

tca gac atc ctc aga tct gca att tgt ttt cca ttt gla ttc aac tct 240
 Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65 70 75 80

gtc aaa aat ggc tct acc tgg act tac ggg act ctg act tgc aaa gtc 288
 Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85 90 95

att gcc ttt ctg ggg gtt ttg tcc tgt ttc cac act gcc ttc atg ctc 336
 Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
 100 105 110

ttc tgc atc agc gtc acc aga tac tta gcc atc gcc cat cac cgc ttc 384
 Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
 115 120 125

tat aca aag agg ctg acc ttt tgg acg tgt ttg gct gtg atc tgc atg 432
 Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
 130 135 140

gtg tgg act ctg tct gtg gcc atg gca ttt ccc cca gtt tta gat gta 480
 Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
 145 150 155 160

ggc acc tac tca ttc att agg gag gag gat cag tgt acc ttc caa cac 528
 Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His
 165 170 175

cgc tcc ttc agg gct aac gat tcc cta gga ttt atg ctg ctc ctt gct 576
 Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala
 180 185 190

ctc atc ctc cta gcc aca cag ctt gtc tac ctc aag ctg ata ttt ttt 624
 Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe
 195 200 205

gtc cac gat cga agg aaa atg aag cca gtc cag ttt gla gca gca gtg 672
 Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
 210 215 220

agt cag aac tgg acc ttt cat ggc cct gga gct agt ggc cag gca gct 720
 Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
 225 230 235 240

gcc aat tgg cta gca gga ttt gga agg ggt ccc aca cca ccc acc ttg 768
 Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu

0022430 084700

19/24

245

250

255

ctg ggc atc agg caa aat gcg aat acc aca ggc aga aga cgg ctc ttg 816
 Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
 260 265 270

gtt ttg gat gag ttc aaa atg gag aaa aga atc agc aga atg ttc tat 864
 Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
 275 280 285

ata atg act ttc ctc ttc cta acc ttg tgg ggt ccc tac ctg gtg gcc 912
 Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
 290 295 300

tgc tat tgg aga gtt ttt gca aga ggg cct gta gta cca ggg gga ttt 960
 Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
 305 310 315 320

cta aca gcc gct gtc tgg atg agt ttc gcc caa gca gga atc aat ccc 1008
 Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
 325 330 335

ttt gtc tgc att ttc tcc aac agg gag ctg agg cgc tgt ttc agc aca 1056
 Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr
 340 345 350

acc ctt ctt tac tgc aga aaa tcc agg tta cca agg gaa cct tac tgt 1104
 Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys
 355 360 365

gtt ata tga 1113
 Val Ile
 370

<210> 24
 <211> 370
 <212> PRT
 <213> Rattus sp.

<400> 24
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 1 5 10 15

Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
 20 25 30

Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35 40 45

Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50 55 60

Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65 70 75 80

0062430 004700

20/24

Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85 90 95
 Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
 100 105 110
 Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
 115 120 125
 Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
 130 135 140
 Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
 145 150 155 160
 Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His
 165 170 175
 Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala
 180 185 190
 Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe
 195 200 205
 Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
 210 215 220
 Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
 225 230 235 240
 Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu
 245 250 255
 Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
 260 265 270
 Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
 275 280 285
 Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
 290 295 300
 Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
 305 310 315 320
 Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
 325 330 335
 Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr
 340 345 350
 Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys
 355 360 365
 Val Ile
 370

002180-0122900

21/24

<210> 25
 <211> 1122
 <212> DNA
 <213> Rat coronavirus

<220>
 <221> CDS
 <222> (1)..(1119)
 <223> Rat SREB3

<400> 25
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 Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
 1 5 10 15

ctg cca tca gca tgc gct tat gtg aag ctg gtg ctg ctg gga ctg atc 96
 Leu Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
 20 25 30

atg tgt gta agc ctg gca ggc aat gcc atc ttg tcc ctg ctg gtg ctc 144
 Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
 35 40 45

aag gag cgt gcc ctg cac aag gct cct tac tac ttt ctg ctg gac ctg 192
 Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
 50 55 60

tgc cta gcc gat ggc ata cgc tct gcc atc tgc ttc ccc ttt gta ctg 240
 Cys Leu Ala Asp Gly Ile Arg Ser Ala Ile Cys Phe Pro Phe Val Leu
 65 70 75 80

gct tct gtg cgc cat ggc tcc tgc tgg acc ttc agt gca ctc agc tgt 288
 Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
 85 90 95

aag att gtg gcc ttt atg gct gtg ctc ttt tgc ttc cat gcg gcc ttc 336
 Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
 100 105 110

atg ctg ttc tgc atc agc gtc acc cgc tac atg gcc atc gcc cac cac 384
 Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
 115 120 125

cgc ttc tat gcc aag cgc atg aca ctc tgg aca tgc gca gct gtc atc 432
 Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
 130 135 140

tgc atg gcc tgg acc ttg tct gtg gcc atg gct ttc cca cct gtc ttt 480
 Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
 145 150 155 160

gat gtg ggc acc tac aag ttt atc cga gag gag gac cag tgc atc ttt 528
 Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
 165 170 175

0062439 081700

22/24

gag cat cgc tac ttc aaa gca aat gac act ctg ggc ttt atg ctt atg 576
 Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
 180 185 190

tig gct gtg ctc atg gca gcc aca cat gct gtc tat ggc aag ctg cta 624
 Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu
 195 200 205

ctc ttc gag tat cgt cac cgc aag atg aag cca gtg cag atg gtg ccc 672
 Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro
 210 215 220

gcc atc agc caa aac tgg aca ttc cat ggc cct ggg gct acc ggc cag 720
 Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln
 225 230 235 240

gct gct gcc aac tgg atc gct ggc ttt ggc cgt ggg ccc atg cca cca 768
 Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro
 245 250 255

act ctg ctg ggt atc cgg cag aat ggg cat gca gct agc cgg cgg cta 816
 Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu
 260 265 270

ctg ggc atg gac gag gtc aag ggt gaa aag cag ctg ggc cga atg ttc 864
 Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe
 275 280 285

tac gcg att aca ctg ctc ttc ctg ctc ctc tgg tca cca tac att gtg 912
 Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val
 290 295 300

gcc tgc tac tgg cga gtg ttt gtg aaa gcc tgc gct gtg ccc cac cgc 960
 Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg
 305 310 315 320

tac ctg gcc act gct gtt tgg atg agc ttc gcc cag gct gct gtc aac 1008
 Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn
 325 330 335

cca atc gtc tgc ttc ctg ctt aac aag gac ctc aag aag tgc ctg agg 1056
 Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Arg
 340 345 350

act cat gcc cct tgc tgg ggc aca gga ggt gcc cca gct ccc aga gaa 1104
 Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu
 355 360 365

ccc tac tgt gtc atg tga 1122
 Pro Tyr Cys Val Met
 370

<210> 26

<211> 373

23/24

<212> PRT

<213> Rat coronavirus

<400> 26

Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
 1 5 10 15

Leu Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
 20 25 30

Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
 35 40 45

Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
 50 55 60

Cys Leu Ala Asp Gly Ile Arg Ser Ala Ile Cys Phe Pro Phe Val Leu
 65 70 75 80

Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
 85 90 95

Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
 100 105 110

Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
 115 120 125

Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
 130 135 140

Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
 145 150 155 160

Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
 165 170 175

Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
 180 185 190

Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu
 195 200 205

Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro
 210 215 220

Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln
 225 230 235 240

Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro
 245 250 255

Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu
 260 265 270

Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe

00622420 001700

24/24

275

280

285

Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val
290 295 300

Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg
305 310 315 320

Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn
325 330 335

Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Arg
340 345 350

Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu
355 360 365

Pro Tyr Cys Val Met
370

00622430 081200